

: protein - protein search, using sw model
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 on: October 22, 2004, 08:38:11 ; Search time 195 Seconds
 (without alignments)
 436.695 Million cell updates/sec

title: US-10-723-368-2
 perfect score: 794
 sequence: 1 MARIPTAALGCGISLICLQLP..... GPAGRQDSAPVDPSSSPHSYG 148
 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 searched: 1825181 seqs, 575374646 residues
 total number of hits satisfying chosen parameters: 1825181

suit No.	Score	Query Length	Match Length	DB	ID	Description
1	794	100.0	148	1	ADM2_HUMAN	Q724h4 homo sapien
2	455	57.3	150	1	ADM2_MOUSE	Q7tnk8 mus musculus
3	451	56.8	146	1	ADM2 RAT	F61312 rattus norvegicus
4	451	56.8	146	2	AAT01302	Aat01302 rattus norvegicus
5	219.5	27.6	168	2	Q75XN7	Q75Xn7 fugu rubripinnis
6	219.5	27.6	168	2	BAD02342	BAD02342 fugu rubripinnis
7	204	25.7	159	2	Q75XN6	Q75Xn6 fugu rubripinnis
8	204	25.7	159	2	BAD02343	BAD02343 fugu rubripinnis
9	201	25.3	140	2	Q6fFS9	Q6fFS9 brachydanius fuscus
10	99	12.5	186	2	Q8NF79	Q8nf79 homo sapiens
11	98.5	12.4	953	2	Q6kT69	Q6kT69 oryza sativa
12	98.5	12.4	953	2	BAD21873	BAD21873 oryza sativa
13	98.5	12.4	953	2	BAD21878	BAD21878 oryza sativa
14	98	12.3	123	2	Q75XW4	Q75Xw4 fugu rubripinnis
15	98	12.3	123	2	BAD02345	BAD02345 fugu rubripinnis
16	98	12.3	1458	2	Q6BJT8	Q6bjt8 debaryomyces hansenii
17	98	12.3	2715	1	ML14_HUMAN	Q9umns6 homo sapiens
18	97.5	12.3	292	2	Q96R16	Q96r16 homo sapiens
19	97.5	12.3	1003	1	MBD6_HUMAN	Q96dn6 homo sapiens
20	97.5	12.3	1003	2	Q6P0F0	Q6p0p0 homo sapiens
21	97.5	12.3	1003	2	AAH65330	AAh65330 homo sapiens
22	97	12.2	174	2	Q75XW8	Q75Xw8 fugu rubripinnis
23	97	12.2	174	2	BAD02341	BAD02341 fugu rubripinnis
24	95.5	12.2	571	2	Q8NB10	Q8nb10 homo sapiens
25	96.5	12.2	1186	2	Q7T401	Q7t401 cercopithecus aethiops
26	96	12.1	406	1	PYG2_HUMAN	Q9brq0 homo sapiens
27	96	12.1	406	2	BAC03877	Bac03877 homo sapiens
28	96	12.1	437	2	Q6Z8R8	Q6z8r8 oryza sativa
29	96	12.1	437	2	BAD10031	Bad10031 oryza sativa
30	95.5	12.0	294	2	Q86TQ3	Q86tq3 homosapiens
31	95.5	12.0	328	2	Q86TQ7	Q86tq7 homosapiens

SUMMARIES

%
 Query Match Length DB ID

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

3.2	95.5	12.0	414	2	Q6M1W2
3.3	95.5	12.0	414	2	CAF20925
3.4	95.5	12.0	571	2	Q6H9L7
3.5	95	12.0	1829	1	Y296_HUMAN
3.6	95	12.0	1832	2	Q8IVD3
3.7	94.5	11.9	201	2	Q9HA0
3.8	94	11.8	155	2	Q8PC51
3.9	94	11.8	171	2	Q6L8K5
4.0	94	11.8	171	2	BAD19046
4.1	94	11.8	756	2	Q6C2Z4
4.2	93.5	11.8	414	2	Q9SEE9
4.3	93.5	11.8	619	2	Q82ILB
4.4	93	11.7	216	2	Q80VAG
4.5	93	11.7	500	1	FXE2_HUMAN

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

total number of hits satisfying chosen parameters:

maximum DB seq length: 0
maximum DB seq length: 200000000

Post-processing: Maximum Match 100%
Listing first 45 summaries

2: uniprot_trembl:*

Pred. No. is the number of results predicted greater than or equal to the score and is derived by analysis of the total.

Result	No.	Score	Match Length	ID	Description	
					DB	DB
	1	794	100.0	148	1	ADM2_HUMAN
	2	455	57.3	150	1	ADM2_MOUSE
	3	451	56.8	146	1	ADM2 RAT
	4	451	56.8	146	2	ADM2 RAT
	5	219.5	27.6	168	2	Q75XW7
	6	219.5	27.6	168	2	BAD02342
	7	204	25.7	159	2	Q75XW6
	8	201	25.7	159	2	BAD02343
	9	201	25.3	140	2	Q6TF59
	10	99	12.5	186	2	Q8NP76
	11	98.5	12.4	953	2	Q8K769
	12	98.5	12.4	953	2	BAD21873
	13	98.5	12.4	953	2	BAD21878
	14	98	12.3	123	2	Q75XW4
	15	98	12.3	123	2	BAD02345
	16	98	12.3	1458	2	Q6BT78
	17	98	12.3	2715	1	MJL4_HUMAN
	18	97.5	12.3	292	2	Q9RY6
	19	97.5	12.3	1003	1	MBD6_HUMAN
	20	97.5	12.3	1003	1	QSF0PO
	21	97.5	12.3	1003	2	ARH6530
	22	97	12.2	174	2	Q75XW8
	23	97	12.2	174	2	BAD02341
	24	96.5	12.2	571	2	Q8NB10
	25	96.5	12.2	1186	2	Q7T401
	26	96	12.1	406	1	PIC2_HUMAN
	27	96	12.1	406	2	BAC03877
	28	96	12.1	437	2	Q5Z8R8
	29	96	12.1	437	2	BAD10031
	30	95.5	12.0	294	2	Q8BTW3
	31	95.5	12.0	328	2	Q8ET07

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RA RA Intermedin is a calcitonin gene-related peptide family
RT RT peptide acting through the calcitonin receptor-like
PT PT activating-modifying protein receptor complexes.”

RL J. Biol. Chem. 279:7264-7274 (2004).

[2] RN SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RC DOI=10.1016/S0014-5793(03)01368-1;
 RX Pubmed=14106835;
 RA Takei Y, Inoue K, Ogoshi M, Kawahara T, Bannai H,
 "Identification of novel adrenomedullin in mammals: a
 RT cardiovascular and renal regulator.";
 RR types TKT ECF2 FGF20001
 PR

RN [3]

RA Clamp M., Smink L.-J., Ainscough R., Almeida J.P., Bab

RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beaumont A.M., Bridgeman A.M., Buck D., Burgoyne C., Bird C.P., Blakey S.E.,

COLLIER, G. COLE, G. COLE, G. COLE, G. COLE, G.

RA Conroy D.; Corby N.R.; Coville G.J.; Cox A.V.; Davis

RA Gilbert J.G.R.; Goward M.E., Grahams D.V., Griffiths

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C.,

RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillips

RA PHILLIPS S.H., PLUMB R.W., RAMSEY H., SMALLER G., SMITH C., SWANSON C.

Soderlund C., RA spragdon L., Sulston J.E., Steward C.A., Sulston J.E.,

RA Vaudin M. Wallis J.M. Whiteley M.N. Williams J.M. Wimberley J.M.

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RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasakawa S., Kuddoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., Roe B.A., Chen F., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hua A., Kenton S., Lai H., Lao H., Lewis J., Lewis S., Lin S.-P., Loh P., Malai E., Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp D., Layman D., Ozeryuk P., Rohlfing T., Scheit P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hillman L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurashiki H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodensteiner A., Hartman K., Hu X., Khan A.S., Lane L., Tilman Y., Wright H.; "The DNA sequence of human chromosome 22."; Nature 402:489-495 (1999).

CC -!- FUNCTION: IMDL and IMD5 may play a role as physiological regulators of gastrointestinal, cardiovascular bioactivities mediated by the CALCR1/RAMPs receptor complexes. Activates the cAMP-dependent pathway.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed in the esophagus, stomach, jejunum, ileum, ileocecum, ascending colon, transverse colon, descending colon and rectum.

CC -!- SIMILARITY: Belongs to the adrenomedullin family.

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CC DR; AF29213; AAQ09100.1; -.

DR EMBL; AB121034; BAD07411.1; -.

DR AL096767; -; NOT_ANNOTATED_CDS.

DR Genew; HGNC:28898; ADM2.

DR MIM: 608682; .

RW Amidation; Cleavage on pair of basic residues; Hormone; Signal.

FT SIGNAL 1 24 Potential.

FT PROPEP 25 98 By similarity.

FT PEPTIDE 101 147 Adrenomedullin 2 (By similarity).

FT PEPTIDE 108 147 Intermedullin-short (Potential).

FT DISULFID 110 115 By similarity.

FT MOD_RES 147 147 Tyrosine amide (G-148 provides amide group) (Probable).

FT SEQUENCE 148 AA; 15865 MW; 6E03098CFC5SBF2 CRC64;

SQ Query Match 100.0%; Score: 794; DB: 1; Length: 148; Best Local Similarity 100.0%; Pred. No. 2.2e-52; Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPTAALGCISLICLQLPGSLSRLSGLDPRPVKPREPARSSSSLQPRHPAPRPPYW 60

DB 1 MARIPTAALGCISLICLQLPGSLSRLSGLDPRPVKPREPARSSSSLQPRHPAPRPPYW 60

QY 61 KHLRQLAQDAGAGAPMQLPQLRQGRGSGPRHSQPRHTQQLRVCVLGTCQVNLI 120

DB 61 KHLRQLAQDAGAGAPMQLPQLRQGRGSGPRHSQPRHTQQLRVCVLGTCQVNLI 120

QY 121 SHRLWQLMGPAGRDPSAQPDPSSPHSYG 148

DB 121 SHRLWQLMGPAGRDPSAQPDPSSPHSYG 148

QY 6 TAALGCISLICLQLPGSLSRLSGLDPRPVKPREPARSSSSLQPRHPAPRPPYWKLHR- 64

DB 8 TIVLGICSLYL-PIGTLSIGLGRHSPRPKFSNLLQGHPLQPTVTKRSRH 66

QY 65 ALQAQRGAGAHAPMQLPQLRQGRGSGPRHSQPRHTQQLRVCVLGTCQVNLSHLR- 124

ADM2_MOUSE ID ADM2 MOUSE STANDARD; PRT; 150 AA.

AC Q7TNK8; i ID ADM2_MOUSE DT 05-JUL-2004 (Rel. 44, Created)

AC Q7TNK8; i ID ADM2_MOUSE DT 05-JUL-2004 (Rel. 44, Last sequence update)

AC Q7TNK8; i ID ADM2_MOUSE DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin (Intermedin-long) (IMD5); Intermedin-short (IMD5)].

DB Name=Adm2; Synonyms=Am2; GN Mus musculus (Mouse).

OS Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

OC

OC

NCBI_TaxID=10090; RN [1]

RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

RC STRAIN=CS7BL/6; RX PubMed=14611540; DOI=10.1074/jbc.M305332200;

RC TISSUE=Kidney; RA Roh J., Chang C.L., Bhaila A., Klein C., Hsu S.Y.T.; RT "Intermedin is a calcitonin/calcitonin gene-related peptide family peptide acting through the calcitonin receptor-like receptor/receptor activity-modifying protein receptor complexes."; RT RL J. Biol. Chem. 279:7264-7274 (2004).

RC TISSUE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

RC TISSUE=Kidney; RX PubMed=14706835; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi N.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent cardiovascular and renal regulator."; RL FEBS Lett. 555:53-58 (2004).

CC -!- FUNCTION: IMD1 and IMD5 may play a role as physiological regulators of gastrointestinal, cardiovascular bioactivities mediated by the CALCR1/RAMPs receptor complexes. Activates the CAMP-dependent pathway.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: High expression detected in the submaxillary gland, kidney, stomach, and mesentery, followed by the pituitary, lung, pancreas, intestines, spleen, thymus and ovary. Expressed mainly in the intermediate lobe of the pituitary, with sporadic in the anterior lobe.

CC -!- SIMILARITY: Belongs to the adrenomedullin family.

CC -!- SUBCELLULAR LOCATION: Secreted.

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CC DR EMBL; AF529212; AAQ09099.1; -.

DR MGDB; AB121033; BAD07412.1; -.

DR MGDB; MG1:267256; Adm2.

DR Amidation; Cleavage on pair of basic residues; Hormone; Signal.

FT SIGNAL 1 25 By similarity.

FT PROPEP 26 100 Adrenomedullin 2 (By similarity).

FT PEPTIDE 103 149 Intermedin-short (Potential).

FT DISULFID 110 117 By similarity.

FT DISTIFID 112 117 By similarity.

FT MOD_RES 149 149 Tyrosine amide (G-150 provides amide group) (Probable).

FT SEQUENCE 150 AA; 16188 MW; 2EFF392BFBDDBA CRC64;

QY Query Match 57.3%; Score: 455; DB: 1; Length: 150; Best Local Similarity 66.0%; Pred. No. 7.2e-27; Matches 95; Conservative 12; Mismatches 35; Indels 2; Gaps 2;

Db 8 TIVLGICSLYL-PIGTLSIGLGRHSPRPKFSNLLQGHPLQPTVTKRSRH

Db	67 APQPQRGNRALAMVHLPGGGSRHGPQRTGSSRRPHAQLLRVGCVLGTCQVNLSHRL 126	Qy	66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124	
	125 WOLMGPAQRDSDAPVDPSSPSHYG 148	Db	64 LQPOQGNGNPALATVHHP-QGGGSRHSRHPQHVGSRPHAQLLRVGCVLGTCQVNLSHRL 122	
Qy	125 WOLVTPAGRDRSAPVDPSSPSHYG 150	Qy	125 WOLMGPAQRDSDAPVDPSSPSHYG 148	
	127 WOLVTPAGRDRSAPVDPSSPSHYG 146	Db	123 WOLVTPAGRDRSAPVDPSSPSHYG 146	
RESULT 3 ADM2 RAT	STANDARD; PRT; 146 AA.	RESULT 4 ADM2 RAT	PRT; 146 AA.	
	AC P61312; ID DT 05-JUL-2004 (Rel. 44, Created) DT 05-JUL-2004 (Rel. 44, Last sequence update) DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2 (Intermedin-long) (IMDL); Intermedin-short (IMDS)]. DE Name=Adm2; Synonyms=Am2; OS Rattus norvegicus (Rat). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Rattus. OX NCBI_TaxID=10116; RN [1] SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent cardiovascular and renal regulator."; RL FEBS Lett. 556:53-58 (2004). RN [2] FUNCTION AND TISSUE SPECIFICITY. RP PubMed=14615490; DOI=10.1074/jbc.M305332200; RA Roh J.; Chang C.L.; Bhalla A.; Klein C.; Hsu S.Y.T.; RT "Intermedin is a calcitonin/calcitonin gene-related peptide family peptide acting through the calcitonin receptor-like receptor/receptor activity-modifying protein receptor complexes."; RL J. Biol. Chem. 279:7264-7274 (2004). CC -!- FUNCTION: IMDL and IMDS may play a role as physiological regulators of gastrointestinal, cardiovascular bioactivities mediated by the CALCRL/RAMPs receptor complexes. Activates the CAMP-dependent pathway. CC -!- SUBCELLULAR LOCATION: Secreted. CC -!- TISSUE SPECIFICITY: Expression was restricted to the intermediate and anterior lobes of the pituitary. CC -!- SIMILARITY: Belongs to the adrenomedullin family. CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;	
RESULT 3 ADM2 RAT	SIGNAL 1 25 Potential. PT PROPEP 26 96 By similarity. PT PEPTIDE 99 145 Adrenomedullin 2 (By similarity). PT PEPTIDE 106 145 Intermedin-short (Potential). PT DISULFID 108 113 By similarity. PT MOD_RES 145 145 Tyrosine amide (G-146 provides amide group) (probable). PT SEQUENCE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	PROTEIN 1 25 Potential. PT PEPTIDE 99 145 Adrenomedullin 2 (By similarity). PT PEPTIDE 106 145 Intermedin-short (Potential). PT DISULFID 108 113 By similarity. PT MOD_RES 145 145 Tyrosine amide (G-146 provides amide group) (probable). PT SEQUENCE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;
RESULT 3 ADM2 RAT	SEQUENCE FROM N.A. RN TISSUE=Kidney; RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1; RA Takei Y.; Inoue K.; Ogoshi M.; Kawahara T.; Barnai H.; Miyano S.; RT "Identification of novel adrenomedullin in mammals: a potent IMD sequence."; RL Submitted (APR 2004) to the EMBL/GenBank/DBJ databases. DR EMBL; AY590103; AAT01302.1; -. DR SEQNCNE 146 AA; 15572 MW; C87043237AD29DDC CRC64;	RESULT 5 ADM2	Qy 6 TAALGGISLCLQLPQSLSSLGQDERPVPREPARSPSSSLQPRHPAPRPTWKLHRA 65 Db 8 TVTFGCISLYL-LFPTLGSIG--KGLRPREPKAPKIPSSGPQCPHPSLRLPPTWKLHRA 63	Query Match 66 LQAO-FGAGLAPVMCGPLRDGGRHSGPRTQAOILRGGVLTGTQOQNLSHRL 124 Best Local Similarity 65.3%; Pred. No. 1.4e-26; Indels 6; Gaps 4; Matches 94; Conservative 13; Mismatches 31; No. 1.4e-26;

Query Match	27.6%	Score 219.5;	DB 2;	Length 168;	OX NCBI_TAXID=31033;
Best Local Similarity	41.1%;	Pred. No.	4.2e-09;		RN [1]
Matches	67; Conservative	21; Mismatches	44;	Indels	31; Gaps
					SEQUENCE FROM N.A. MEDLINE=22984567; PubMed=14623291;
2Y	12 ISHLQIPLG-SLRSLGDP-----RPyK-PREP-----PARFSSSIQPRHPAPRP- 11 ISLIPLEQARALLQNLGLPFRFLSLRTIKPKSSFIVGPAASDPPETVYHQAQGDG 70				RA Ogoshi M.; Inoue K.; Takei Y; RT fish."; RT Biochem. Biophys. Res. Commun. 311:1072-1077(2003). DR EMBL: AB120297; BAD0243.1; -. SQ SEQUENCE 159 AA; 18028 MW; F1863B20100E254D CRC64;
Db					
2Y	58 -YWWKLHLAQORGAGLA---PYMGQP---LRD---GGQRHSGPFRH--SGPRRTOAQL 105 71 RYTW----MAWLKGKPLIPLGSDDPLQGTDRLTPANGRSRGRHANGGGRSHGQL 125				Query Match 25.7%; Score 204; DB 2; Length 159; Best Local Similarity 34.8%; Pred. No. 5.8e-08; Matches 62; Conservative 16; Mismatches 32; Indels 68; Gaps 9;
Db					
2Y	106 IRYVCVLGTCQVONLSHRLWQLMGPGRQDSAPVDPSSPSYG 148 126 MRYACVLGTCQVONLSHRLQIGSKEDSPMNPHSPHSYQ 168				Qy 11 CTSILCLC-----QLP-----GSLSRSLGG-DPRPVKPREPAPRSPS 45 Db 10 CTSILSLPLRLETLPAAEPDENRLLDIDQRDKSSVSQKNNDVPP-----A 59
Db					
RESULT 6					
BAD02342	BAD02342; PRELIMINARY;	PRT;	168 AA.		Qy 46 SSIQPR-----HPAPRPVWKL-----HRAIAQORGAGLAIVMGQPLRDGRQS-QHS- 90 Db 60 SSISPKWLSKHSGTHSGVKVRLSLAWARPQRRLFRARR-----EHHSR 103
AC					
DT	14-APR-2004 (TREMBLrel. 27, Created)				
DT	14-APR-2004 (TREMBLrel. 27, Last sequence update)				
DT	14-APR-2004 (TREMBLrel. 27, Last annotation update)				
DE	Adrenomedullin-2.				
DN	ADM2.				
DS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
DC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
DC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
DC	Tetraodontiformes; Tetraodontidae; Takifugu.				
DN	Adrenomedullin-3.				
GN	NCBI_TAXID=31033;				
GT	Ogoshi M.; Inoue K.; Takei Y;				
RT	"Identification of a novel adrenomedullin gene family in teleost fish."				
RT	Biochem. Biophys. Res. Commun. 311:1072-1077(2003).				
DR	EMBL: AB120296; BAD0242.1; -.				
SQ	SEQUENCE 168 AA; A5905E7CC112669B CRC64;				
Query Match	27.6%; Score 219.5;	DB 2;	Length 168;		
Best Local Similarity	41.1%;	Pred. No.	4.2e-09;		
Matches	67; Conservative	21; Mismatches	44;	Indels	31; Gaps
					SEQUENCE FROM N.A. MEDLINE=22984567; PubMed=14623291;
2Y	12 ISHLQIPLG-SLRSLGDP-----RPyK-PREP-----PARFSSSIQPRHPAPRP- 11 ISLIPLEQARALLQNLGLPFRFLSLRTIKPKSSFIVGPAASDPPETVYHQAQGDG 70				RA Ogoshi M.; Inoue K.; Takei Y; RT fish."; RT Biochem. Biophys. Res. Commun. 311:1072-1077(2003). DR EMBL: AB120297; BAD0243.1; -. SQ SEQUENCE 159 AA; 18028 MW; F1863B20100E254D CRC64;
Db					
2Y	58 -YWWKLHLAQORGAGLA---PYMGQP---LRD---GGQRHSGPFRH--SGPRRTOAQL 105 71 RYTW----MAWLKGKPLIPLGSDDPLQGTDRLTPANGRSRGRHANGGGRSHGQL 125				Query Match 25.7%; Score 204; DB 2; Length 159; Best Local Similarity 34.8%; Pred. No. 5.8e-08; Matches 62; Conservative 16; Mismatches 32; Indels 68; Gaps 9;
Db					
RESULT 7					
275XW6	Q75XW6; PRELIMINARY;	PRT;	159 AA.		Qy 11 CTSILCLC-----QLP-----GSLSRSLGG-DPRPVKPREPAPRSPS 45 Db 10 CTSILSLPLRLETLPAAEPDENRLLDIDQRDKSSVSQKNNDVPP-----A 59
AC					
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DE	Adrenomedullin-3.				
DN	Name=ADM3;				
DS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
DC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;				
DC	Tetraodontidae; Takifugu.				
GT	Ogoshi M.; Inoue K.; Takei Y;				
RT	"Identification of a novel adrenomedullin gene family in teleost fish."				
RT	Biochem. Biophys. Res. Commun. 311:1072-1077(2003).				
DR	EMBL: AB120297; BAD0243.1; -.				
SQ	SEQUENCE 159 AA; 18028 MW; F1863B20100E254D CRC64;				
Query Match	27.6%; Score 219.5;	DB 2;	Length 168;		
Best Local Similarity	41.1%;	Pred. No.	4.2e-09;		
Matches	67; Conservative	21; Mismatches	44;	Indels	31; Gaps
					SEQUENCE FROM N.A. MEDLINE=22984567; PubMed=14623291;
2Y	106 IRYVCVLGTCQVONLSHRLWQLMGPGRQDSAPVDPSSPSYG 148 126 MRYACVLGTCQVONLSHRLQIGSKEDSPMNPHSPHSYQ 168				RA Ogoshi M.; Inoue K.; Takei Y; RT fish."; RT Biochem. Biophys. Res. Commun. 311:1072-1077(2003). DR EMBL: AB120297; BAD0243.1; -. SQ SEQUENCE 159 AA; 18028 MW; F1863B20100E254D CRC64;
Db					
RESULT 9					
Q6IFS9	Q6IFS9; PRELIMINARY;	PRT;	140 AA.		
ID					
DC					
DC					

AC Q6IFS9;	Db 122 PLYLTHSPRLHQSTQAQVPAFLYSQTWEQDDMMKTTQTPLSRRS--	GVC--RGADRLLWK 176
DT 05-JUL-2004 (TREMBLrel. 27, Created)	QY 127 LMG-PAG 132	
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	DB 177 LQGLPLG 183	
DR Intermediate (Fragment).		
GN Name=IMDN;		
OS Brachydanio rerio (Zebrafish) (Danio rerio).		
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC Cyprinidae; Danio.		
OX NCBI_TaxID=7955;		
RN [1]		
SEQUENCE FROM N.A.		
PubMed=14165490;		
RA Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.;		
RT "Intermelein is a calcitonin/CGRP family peptide acting through the CRL/RAMP receptor complexes.";		
RL J. Biol. Chem. 0:0-0(2003).		
RN [2]		
SEQUENCE FROM N.A.		
RP Hsu S.Y.T.;		
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.		
CC -!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DBJ third party annotation (TPA) entry.		
DR EMBL; BK004089; DAA045551; -.		
FT NON_TER 1_1;		
SQ SEQUENCE 140 AA; 15816 MW; 509F74908C0DC75D CRC64;		
Query Match 25.3%; Score 201; DB 2; Length 140;		
Best Local Similarity 40.2%; Pred. No. 8.7e-08;		
Matches 47; Conservative 11; Mismatches 31; Indels 28; Gaps 3;		
QY 32 RPVKPKEPPARPSQSSLIQPRHPAPRPPVWKLHRAQAGKGLAPVNGQPLURDGERQHSG 91		
Db 52 RAILSSAPPADLTGQNQLQSTYLESP ----- KQERRRHVV 86		
QY 92 PRRHSGPRTTQDQLLRVGCVLGTQVONLSHRLWOLMGPAQRQDSAPVDPSSPHSYG 148		
Db 87 SRGHHS--HHEFQLMRYGVQVNLSHRLWLYQNGSREDS-PINPPSPHSGV 140		
RESULT 10		
QBNT76 ID Q8NF76 PRELIMINARY; PRT; 186 AA.		
AC Q8NF76;		
DT 01-OCT-2002 (TREMBLrel. 22, Created)		
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)		
DR FLJ00287 protein (Fragment).		
DE Name=FLJ00287;		
GN Homo sapiens (Human).		
OS Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Primates; Catarrhini; Hominoidea; Homo.		
NCBI_TaxID=9606;		
RN [1]		
SEQUENCE FROM N.A.		
RC TISSUE=Spleen;		
RA Jikuya H., Takano J., Kituno R., Nagase T., Ohara O.;		
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.		
DR EMBL; AK050403; BAC03384.1; -.		
FT NON_TER 1_1;		
SQ SEQUENCE 186 AA; 20177 MW; 85ADCFC5B8106CD4 CRC64;		
Query Match 12.5%; Score 99; DB 2; Length 186;		
Best Local Similarity 31.5%; Pred. No. 5.3;		
Matches 40; Conservative 9; Mismatches 48; Indels 30; Gaps 10;		
QY 29 G DPRPVKPR-----EPPARPSQSSLIQPRH--PAPRPPVWKLHRAQAGKGLA 75		
Db 64 GSPLIPASPHPPHQPPAPFDPPTRSPDPAVSSAHSFPAAP--LAWSCVTLHSPLSLPL-SKLP 121		
QY 76 P--VMGQPLRDGRQHSGPRRH-----SGPRTTAQQLRVCULGTCVQVNLSERLWK 126		

Db 118 PQGYG 122

Search completed: October 22, 2004, 08:54:32
Job time : 201 secs

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OM protein - Protein search, using sw model

Run on: October 22, 2004, 08:46:21 ; Search time 40 Seconds
(without alignments)

Title: US-10-723-368-2
Perfect score: 794

Sequence: 1 MARIPTAALGCTISILCQLP.....GPAGRQDSAPVDPSSPHSYG 148
Scoring table: Blosum62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters:

478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Issued_Patents_AAI:
1: /cgn2_6_ptodata/1/iaa/5A COMB.pep *
2: /cgn2_6_ptodata/1/iaa/5B COMB.pep *
3: /cgn2_6_ptodata/1/iaa/6A COMB.pep *
4: /cgn2_6_ptodata/1/iaa/6B COMB.pep *
5: /cgn2_6_ptodata/1/iaa/PETUS COMB.pep *
6: /cgn2_6_ptodata/1/iaa/backfile1..pep :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	13.9	379	4	US-09-252-991A-26924 Sequence 26924, A Sequence 31641, A Sequence 28208, A Sequence 30685, A Sequence 21581, A Sequence 24041, A Sequence 30948, A Sequence 18286, A Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
2	108	13.6	362	4	US-09-252-991A-21973 Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
3	107.5	13.5	514	4	US-09-252-991A-38208 Sequence 28208, A Sequence 30685, A Sequence 21581, A Sequence 24041, A Sequence 30948, A Sequence 18286, A Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
4	103.5	13.0	621	4	US-09-252-991A-30820 Sequence 28208, A Sequence 30685, A Sequence 21581, A Sequence 24041, A Sequence 30948, A Sequence 18286, A Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
5	103	13.0	142	4	US-09-252-991A-21581 Sequence 21581, A Sequence 24041, A Sequence 30948, A Sequence 18286, A Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
6	102.5	12.9	417	4	US-09-252-991A-24041 Sequence 24041, A Sequence 30948, A Sequence 18286, A Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
7	101	12.7	327	4	US-09-252-991A-30828 Sequence 28208, A Sequence 30685, A Sequence 21581, A Sequence 24041, A Sequence 30948, A Sequence 18286, A Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
8	100.5	12.7	528	4	US-09-252-991A-18286 Sequence 18286, A Sequence 21581, A Sequence 24041, A Sequence 30948, A Sequence 18286, A Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
9	100	12.6	464	4	US-09-252-991A-25833 Sequence 21581, A Sequence 24041, A Sequence 30948, A Sequence 18286, A Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
10	100	12.6	783	4	US-09-252-991A-18035 Sequence 18035, A Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
11	99.5	12.5	763	4	US-09-252-991A-30146 Sequence 30146, A Sequence 24967, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
12	99	12.5	373	4	US-09-252-991A-24961 Sequence 24961, A Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
13	98.5	12.4	588	4	US-09-252-991A-30690 Sequence 30690, A Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
14	98.5	12.4	176	4	US-09-252-991A-30542 Sequence 30542, A Sequence 23976, A Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
15	98.5	12.4	275	4	US-09-252-991A-33976 Sequence 33976, A Sequence 21418, A Sequence 31915, A
16	98.5	12.4	362	4	US-09-252-991A-31016 Sequence 31016, A Sequence 19922, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
17	98.5	12.4	364	4	US-09-252-991A-19923 Sequence 19923, A Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
18	98.5	12.4	498	4	US-09-252-991A-21973 Sequence 21973, A Sequence 24757, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
19	98.5	12.4	642	4	US-09-252-991A-24767 Sequence 24767, A Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
20	98.5	12.4	642	4	US-09-252-991A-32104 Sequence 32104, A Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
21	98	12.3	266	4	US-09-252-991A-30538 Sequence 30538, A Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
22	97.5	12.3	142	4	US-09-252-991A-16714 Sequence 16714, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
23	97.5	12.3	416	4	US-09-252-991A-24575 Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
24	97.5	12.3	436	4	US-09-252-991A-17764 Sequence 17764, A Sequence 24575, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
25	97	12.2	317	4	US-09-252-991A-21126 Sequence 21126, A Sequence 317, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
26	97	12.2	653	4	US-09-252-991A-21418 Sequence 21418, A Sequence 653, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A
27	97	12.2	720	4	US-09-252-991A-31915 Sequence 31915, A Sequence 720, A Sequence 436, A Sequence 31117, A Sequence 31126, A Sequence 21418, A Sequence 31915, A

RESULT 1
US-09-252-991A-26924
; Sequence 26924, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenstein et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196 136
; CURRENT APPLICATION NUMBER: US/09-252-991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-26924
Query Match 13.9%; Score 110; DB 4; Length 379;
Best Local Similarity 29.2%; Pred. No. 0.0026;
Matches 50; Conservative 15; Mismatches 56; Indels 50; Gaps 8;
QY 4 IPTAAAGCISLIC-----IQLPGLSLSRLGAPDPRVPPREPPARSPS 45
Db 70 LPHVGLGRPILLAVGHRPADHYTHRLHQGTAVRLQHGAARPA 129
QY 46 SSL-----QPHHPAPRPVWVHLRHALQAQRGAGLAPMGPQLRDLGRQHSQPRHSG 97
Db 130 RRLYVRLLGREGPDRALULSALYHRP-PATIGHGIQ-----RQERAPGRHAG 177
QY 98 PRTOAQALLRVGCYTGCOYQNLSHLRWLQPMGPAGRDQAPVDISSPHYG 148
Db 178 HQRHAG-----DLGWCRQLRPA-RLPSVAAP----RHPVDPFGGLH RPG 216
RESULT 2
US-09-252-991A-31641
; Sequence 31641, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenstein et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196 136
; CURRENT APPLICATION NUMBER: US/09-252-991A
; CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 SEQ ID NO: 31641
 LENGTH: 362
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-232-991A-31641

Query Match 13.6%; Score 108; DB 4; Length 362;
 Best Local Similarity 32.9%; Pred. No. 0.004; Indels 44; Gaps 10;
 Matches 50; Conservative 16; Mismatches 42; SEQ ID NOS: 33142

QY 17 LQFGSLSSS--LGQDPPEVKP-----REPP---PARSPSS- 47
 Db 206 LRERLNLAIRTRCAAGLPRPRAPGRGROMARPGRRGAPGQPADWRRPAPCGRGTPVVAR 265

QY 48 -LQPRHAPRPPVWKHLRQLAQORGAGLAPVMQGQPLRGROHSQPRHSGPRRTQAOI 105
 Db 266 RDLRPEYGAQPRPAIRRRLR-RADHGATAA---GCVAGAESQRPASGPQ---PRARAGR 317

QY 106 LRVCGVLTGTCQVNLSHLRILWLMGPAGRCDSA 137
 Db 318 RQAGQV-GKDQQPOSRR--LPGP-GRAPGA 344

RESULT 3
 US-09-252-991A-28208
 ; Sequence 28208, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 28208
 ; LENGTH: 514
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-28208

Query Match 13.5%; Score 107.5; DB 4; Length 514;
 Best Local Similarity 27.7%; Pred. No. 0.005; Indels 79; Gaps 11;
 Matches 54; Conservative 11; Mismatches 51; SEQ ID NOS: 33142

QY 20 PGSLRSL-----GCDPR---PVKREPPARS---PSSLQP-- 50
 Db 178 PGFRRALPRLQTAEDRDKKGAAAPAGADPRAAYGFPROPPNGRCLALPGSILRPAG 237

QY 51 -RHPAPRPPVWKHLRQLAQORGAGLAPVMQG-----PLRDGGRQH---SGPR 93
 Db 238 EHHQGP-----CRAPCQREGRVLPAGGQAVHDAAPRTRPELRAAGRRHWRLLQAPG 290

QY 94 RHSGPRTQAOQLRVGCVLT-----CQVNLSHLRQL-----LMGPAG 132
 Db 291 AAVERCGRQLARALPAAGAGPPVAFRAPGAPGCRGRGLSPLRQGAFRPGHQ-AL 349

QY 133 RDSSA---PVDPSS 143
 Db 350 RDDAERGAWPILDPTT 364

; Sequence 30689, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 30689
 ; LENGTH: 621
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-30689

Query Match 13.0%; Score 103.5; DB 4; Length 621;
 Best Local Similarity 28.4%; Pred. No. 0.022; Indels 43; Gaps 7;
 Matches 40; Conservative 13; Mismatches 45; SEQ ID NOS: 33142

Qy 31 PRPTKPREPPARPSSSILQPRHPPAPRPPVWKHLRQLAQORGAGLAPVMQGQPLRGGR--- 87
 Db 421 PDPARTQOPP-ROWLIAVAGQRERPV----ESRPAHQPAAP--GPIRAGALY 472

Qy 88 -QHSQPRBHSQPRERTQQLRIVGCVLGTQCNQVQNL--SHRLWQI----- 127
 Db 473 PGECIAAERHEADPRP-----GTAACQRLAASRLQHASAARPAAGNRRAGD 520

Qy 128 MGPAQRDQDAPVDDSSPHSYG 148
 Db 521 LPPGRRHRVHAAPAPRTG 541

RESULT 5
 US-09-252-991A-21581
 ; Sequence 21581, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 21581
 ; LENGTH: 142
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-21581

Query Match 13.0%; Score 103; DB 4; Length 142;
 Best Local Similarity 39.3%; Pred. No. 0.0043; Indels 34; Gaps 7;
 Matches 35; Conservative 6; Mismatches 34; SEQ ID NOS: 33142

Qy 25 RSLGSDP---RPVKKPREPPARPSSSILQPRH---PAP-REVWVLUHLQALQQR-GAGLAP 76
 Db 11 RTGGCGPAQRLAQPRRPP--PGCACQRRRLPAPERPRWNRHRRTAGAVGRAVLP 67

Qy 77 VMGQPLRDGRQHSG---PRHSGSPRTQA 103
 Db 68 -RTQEQQGTRGPGRPGRPRHAPRPA 95

US-09-252-991A-24041
*; Sequence 24041, Application US/09252991A
; Patent No. 6551795*
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094, 190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 24041
LENGTH: 417
TYPE: PRT
ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-24041
Best Local Similarity 12.9%; Score 102.5; DB 4; Length 417;
Matches 36; Conservative 8; Mismatches 58; Indels 27; Gaps 3;

Qy 20 PGSSLSGCDPRPKPDRPPRSPSSSLQRPHAPRPVWKLHRAHQAGLAPYM 78
Db 216 PGSGTHRALYGDHPHPAGSSADAAPSQRAPAHPVCPARRLSTGGCKPGCRFRPGI 275
Qy 79 -----GQPDRDGGHQHSGPRRHSRRHSSPRRTQAOQLRVGCTGTCAVNLSHRLWQMGPAQ 132
Db 276 PRSAPGHPVSRGPDPGDRRPLHPRR-----HQQRRRRAPD 315
Qy 133 RDQSAFVDP 141
Db 316 PGRLLPVVRP 324

RESULT 7
US-09-252-991A-30948
Sequence 30948, Application US/09252991A
Patient No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094, 190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 30948
LENGTH: 327
TYPE: PRT
ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-30948
Best Local Similarity 12.7%; Score 101; DB 4; Length 327;
Matches 54; Conservative 15; Mismatches 58; Indels 52; Gaps 11;

Qy 11 CTSLICLOPGSLRSLSLGGDRPVK-----PREPPARSPSS-----46
Db 55 CLPLRRRTGTAAGQPGGGPAKVAAGGAGRREPVAVLRARPLAPGRAPGAGDRRR 114
Qy 47 ----SLQPHPA---PRPTWKLHRA-LQAQGAGIA-PVMQOLRQGRHSQG--PR 93
Db 115 GRALSQPRRAAGCQEOP-----HRAGLFAARRAGLACPPATSRRLAAGRRCYHGLPA 169
Qy 94 RHSG----DRTTQQLLRVGCVLGTCQYONLSHRLWQMGPAQDSAPVD--PSSP 144

Db 170 VEPGLIYQPTRIDRALVRYLPRGRCAALRPRRTAAVAG-AGRA-AREVDGQWGP 226
RESULT 8
US-09-252-991A-18286
Sequence 18286, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094, 190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 18286
Query Match 12.7%; Score 100.5; DB 4; Length 528;
Best Local Similarity 28.0%; Pred. No. 0.036;
Matches 47; Conservative 9; Mismatches 43; Indels 69; Gaps 9;
Qy 28 GGDPRPVKP-----REPPARSPSSSLQ---PRHAPAPRVWKLHRA 66
Db 52 GDDPVAADPERGAWMPGHDPAGGDLRQAAAFLGLRHPAVYLHRRR 111
Qy 67 QAQ-----RGAGLAPMGPOL-DGG---RHQSPPRHSGPRRT 101
Db 112 QPECHTRPGLSQRVTLPRRLQLEHGGLRP---QHLRLHDGNLRRDQEHAPRSGSGARLR 168
Qy 102 QAQL-----LRVCGVLGTCQVONLS-----HRLWQLMGPA 131
Db 169 HGRLLHPLPAHRLPAAGTAVLQORSDDAFAFHIGGVHR-HSAGPA 214
RESULT 9
US-09-252-991A-25833
Sequence 25833, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094, 190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 25833
Query Match 12.6%; Score 100; DB 4; Length 464;
Best Local Similarity 28.4%; Pred. No. 0.035;
Matches 42; Conservative 13; Mismatches 47; Indels 46; Gaps 9;
Qy 29 GDP-RPKV-----PREPPARSPSSLQPRHPA-----PRPVWKLHRAQOARGA 72
Db 185 GDPHRPGRVPGPADAAPAAGRDQPROGDRHGAAGAVAGHPAPAVRLHLSQRHGP 244

Qy 73 GLAPVMGGPLR-----DGGRGQSGPRTQAGLRLVCGVLGTCQVNLS 121
 Db 245 ARG----REVVRQAGDAPARAPDPGRH---RRNGLRLR--RRQLPR-----PVESTD 290

Qy 122 HRLW----QLMGAGRQDOSAVPDPS 144
 Db 291 RRAWFGRHRLEPEFGRGHPAYHGP 318

RESULT 10
 US-19-252-991A-18035
 ; Sequence 18035, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 18035
 ; LENGTH: 783
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18035

Query Match 12.6%; Score 100; DB 4; Length 783;
 Best Local Similarity 27.2%; Pred. No. 0.064;
 Matches 44; Conservative 12; Mismatches 56; Indels 50; Gaps 7;

Qy 19 LPGSTLSRSLGDPDVPKPDRPPA--RSPESLSDPDRHPAPRPVVKLHRLQAORGAGIA 75
 Db 3 LPTAPRSPRSQADROTEPARPPAAGRVRVPAQGLGRGRAVQERP-----AGLR 48

Qy 76 PVMGQPLRDGROSGPQR--HSQSPRTQAGLRLVCGLPT--CCYQVNLSH 122
 Db 49 PCL---LHPQGQQRADPLRVAEPARPARTGLAREAGKGKAREDLAVRGTRRLPVDRYR 105

Qy 123 RIWLQLMGPA-----GRODSAPVDPSSPHY 147
 Db 106 RAGRRRPAFLGLRTIEGKTRRRPVRQRTQASAARPSAPHY 147

RESULT 11
 US-09-252-991A-30146
 ; Sequence 30146, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; LENGTH: 763
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-30146

Query Match 12.5%; Score 99.5; DB 4; Length 763;
 Best Local Similarity 25.7%; Pred. No. 0.07; Mismatches 12; Indels 72; Gaps 8;

Qy 3 RIPPAAALGCGISLCLQLPSSLSRSLIG-----GDPFPRV----KPREPPARS 43
 Db 10 RRTPAP-GLVAAALLAWPARRRTGGERAAGAASPATAPGGPVAPAPRHRHCPHPAYA 68

Qy 44 PSSSLQPRHPA----PREVWWKLHRLQAOQRGGLAPWNGQPIRDGGRHQHSGRHSCP 98
 Db 69 PDRSLPAAGPAAARRPRPGAGGCR--RARRGGTAAERRKEEDAAAGRGSAWQRHGEL 126

Qy 99 RR----TOQQLL----RVGCCVLGTCQVNLS 121;
 Db 127 RQVLPAGAGRRIQRQLARTLVIRPAQALAFFURGHRRGQRPGRGLGTRHAGLR 186

Qy 122 HR----IWQLMGPAGRQDSDAPVDPSSP 144
 Db 187 PRGAQRGVTHPVDQRQRSPGDRRRCPADHARP 220

RESULT 12
 US-09-252-991A-24961
 ; Sequence 24961, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 24961
 ; LENGTH: 373;
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24961

Query Match 12.5%; Score 99; DB 4; Length 373;
 Best Local Similarity 31.4%; Pred. No. 0.034;
 Matches 44; Conservative 10; Mismatches 46; Indels 40; Gaps 8;

Qy 24 SRSLGGDPDPVKPDRPPARSPSSLIQPRHPA--PRPVWVKLHRLQAORGAGIAPVMGQP 81
 Db 93 ARLGAEAVNPARP--PPGARRSGTHRPLAEDARPL-----ACHADPSHGTAPHRAYP 144

Qy 82 LRDGGRQHS----GPRHE-SGPRR----TOAQLRYGVCLUSTCQVNLSH 123
 Db 145 ASPPGRRGQOLPPYARRGAEGPRRAAGRDRSGCDRRAPLRQGVQLQPC-LQALE-- 201

Qy 124 IWQLMGPAGRQDSDAPVDPSS 143
 Db 202 -----RHDAAPVSPAA 212

RESULT 13
 US-09-252-991A-30690
 ; Sequence 30690, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30690
; LENGTH: 588
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US -09-252-991A-30690

Query Match 12.5%; Score 99; DB 4; Length 588;
Best Local Similarity 28.9%; Pred. No. 0.058; Gaps 9;
Matches 48; Conservative 10; Mismatches 46; Indels 62; Gaps 9;

QY 21 GSLSRIGGDP-RPVKP-----REPPARSPSSQLQPRHP-----A 54
Db 266 GADGRELLGNEAPREPGLTLAHPQAARRRRPAPRPLALVRHPRAGLQ 325
Qy 55 PRPVVWKLHRAAQDQGAGIAAPVMGOLRIDGRHSQPR----HSG-----PRR 100
Db 326 PRP-----QRSGQAPDRRGQGHHLHARGEQAAREPTPLPHAGKXQRRDLHRR 376
Qy 101 TOAQOLLRVGCYVLGTCTOYNLNSHLRLWQLMG-----PAGRDQAPVPD 141.
Db 377 TQRQRQ---PLGTAEV---RLQFGMGAQRPSPSDRHOPAPRP 414

RESULT 14
; Sequence 30542, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 3342
; SEQ ID NO 30542
; LENGTH: 176
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US -09-252-991A-30542

Query Match 12.4%; Score 98.5; DB 4; Length 176;
Best Local Similarity 31.8%; Pred. No. 0.016; Gaps 8;
Matches 47; Conservative 6; Mismatches 50; Indels 45; Gaps 8;

QY 31 PRPVPREPARSPSSQLQPRHPAP--RPVWKLHRAQORGAGIA-----75
Db 40 PRPV-----PARQEPFRRSQCHPAPLPRG---HRARRARLAAAQRRAAAGPAGR 91
Qy 76 -----PVMDQPLRQDGROSSGP--RHSGSPRTOAQLRV-----GCVLGTCQV 117
Db 92 RLRSHRPRRQQLR---RQQLPAAASRRGCRTRNRQASRQPQPGGATGRPQR 148
Qy 118 QNLSHRLWQNGPAG-RQDSAPVPDSP 144
Db 149 RRLCRRGRRLERAAGPRPAAPLDPGRP 176

RESULT 15
; Sequence 23976, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

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Result No.	Score	Query	Match	Length	DB ID	Description
1	794	100.0	148	17	US-10-723-368-2	Sequence 2, Appli
2	254	32.0	47	17	US-10-723-368-2	Sequence 5, Appli
3	108.5	13.7	311	16	US-10-437-163-202661	Sequence 202661,
4	106.5	13.4	386	15	US-10-425-114-56462	Sequence 56462, A
5	105	13.2	413	16	US-10-437-963-109275	Sequence 109275,
6	103	13.0	556	15	US-10-425-114-65154	Sequence 64514, A
7	101.5	12.8	179	16	US-10-767-701-55404	Sequence 35444, A
8	101	12.7	242	15	US-10-450-436-28	Sequence 28', Appli
9	99.5	12.5	203	16	US-10-767-701-34727	Sequence 34727, A
10	99.5	12.5	19662	15	US-10-084-846A-6	Sequence 6, Appli
11	98.5	12.4	851	16	US-10-437-963-192117	Sequence 192117,
12	98.5	12.4	19695	15	US-10-084-846A-3	Sequence 3, Appli
13	98	12.3	2527	16	US-10-408-765A-2462	Sequence 2462, Ap

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	794	100.0	148	17	US-10-723-368-2	Sequence 2, Appli
2	254	32.0	47	17	US-10-723-368-2	Sequence 5, Appli
3	108.5	13.7	311	16	US-10-437-163-202661	Sequence 202661,
4	106.5	13.4	386	15	US-10-425-114-56462	Sequence 56462, A
5	105	13.2	413	16	US-10-437-963-109275	Sequence 109275,
6	103	13.0	556	15	US-10-425-114-65154	Sequence 64514, A
7	101.5	12.8	179	16	US-10-767-701-55404	Sequence 35444, A
8	101	12.7	242	15	US-10-450-436-28	Sequence 28', Appli
9	99.5	12.5	203	16	US-10-767-701-34727	Sequence 34727, A
10	99.5	12.5	19662	15	US-10-084-846A-6	Sequence 6, Appli
11	98.5	12.4	851	16	US-10-437-963-192117	Sequence 192117,
12	98.5	12.4	19695	15	US-10-084-846A-3	Sequence 3, Appli
13	98	12.3	2527	16	US-10-408-765A-2462	Sequence 2462, Ap

SEQ ID NO.	SEQUENCE
1	MARITAAALGCISLCLQLPGSLSRSLGDPYKPREPPARSPLSQDRPHAPRPPVW
2	1 MARITAAQAGGLAPVMGQLRDRGGROHSGRHSGPRRTQAQLLRVGCVLGTQCQVNQ
3	1 MARITAAALGCISLCLQLPGSLSRSLGDPYKPREPPARSPLSQDRPHAPRPPVW
4	1 MARITAAQAGGLAPVMGQLRDRGGROHSGRHSGPRRTQAQLLRVGCVLGTQCQVNQ

ALIGNMENTS
RESULT 1 US-10-723-368-2
; Sequence 2, Application US-10733368
; Publication No. US20040204353A1
; GENERAL INFORMATION:
; APPLICANT: Sheau Yu Teddy HSU
; TITLE OF INVENTION: Intermedin and Its Uses
; FILE REFERENCE: STAN-284
; CURRENT APPLICATION NUMBER: US-10-723-368
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 601429, 327
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSSQ for Windows Version 4.0
; SEQ ID NO. 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; FEATURE: ;
; NAME/KEY: PEPTIDE
; LOCATION: (1) ... (23)
; OTHER INFORMATION: Mature peptide
US-10-723-368-2

RESULT 2
US-10-723-368-5
*; sequence 5, Application US/10723368
 ; Publication No. US20040204353A1
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: Intermediates and Its Uses
 ; FILE REFERENCE: STAN-284
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIORITY NUMBER: 601429, 327
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 5
 ; LENGTH: 47
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 US-10-723-368-5*

Query Match 32.0%; Score 254; DB 17; Length 47;
 Best Local Similarity 100.0%; Prod. No. 1..e-13;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 TOAQQLRVCVLTGTCQVNQLSHRLWLMGPAGRODSAPVDPSSPHSY 147
 Db 1 TOAQQLRVCVLTGTCQVNQLSHRLWLMGPAGRODSAPVDPSSPHSY 47

RESULT 3
US-10-437-963-202661
*; Sequence 202661, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(5321)B
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 202661
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1) (311)
 ; OTHER INFORMATION: unsure at all xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_9791C.1.pep
 US-10-437-963-202661*

Query Match 13.7%; Score 108.5; DB 16; Length 311;
 Best Local Similarity 27.7%; Prod. No. 0.5;
 Matches 44; Conservative 13; Mismatches 67; Indels 35; Gaps 8;

Qy 48 PAGILRSPGPSPAPASPPASPCHRHRPRPPRRPERRPRPERRPLWLWPS 107
 Qy 65 ALQDQAGGLA-----PVMGCPFLDGRGNGSPRHSG-----PRRT-QAQLRV 108
 Db 108 SLPPTXGBEPWTAAAFPPSPLSLSPRLR--RAYGRRPXPXGAGAASRRRPRXGRARRV 164
 Qy 109 GCVLGTCTQVNQLSHRLWLMGPAGRODSAPVDPSSPHSY 147
 Db 165 AAAWGPA-VSRPRERPVWLTRGAGCAGRXSPGACPAPPWTH 202

RESULT 4
US-10-445-114-56462
*; Sequence 56462, Application US/10425114
 ; Publication No. US2004034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425, 114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO: 56462
 ; LENGTH: 386
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLB73224A12_FLI.pep
 US-10-445-114-56462*

Query Match 13.4%; Score 106.5; DB 15; Length 386;
 Best Local Similarity 28.1%; Prod. No. 0.91; Mismatches 41; Indels 61; Gaps 9;
 Matches 45; Conservative 13; Mismatches 41; Indels 61; Gaps 9;

Qy 1 MARPTAACLGISLCLQLPGSLSRLGGDPRPYKPREPPARS-PSSSLQPRHAP---- 55
 Db 98 LPRLDPLVRKG-----LPRGDRAAAPPD-PPPRERPRRPLRLQPRERSPLPA 148
 Qy 56 --RQVWKI-----HR----ALQRAAGLAGLAPMGQPP-----RDGER 87
 Db 149 RRRRRWLLLSRRHRQQLRAVLRRGGYGPAPPAGHENYLPHGIRLAAGAAGPDGSR 208
 Qy 88 QHSG---PRRHSG-----PRRT-QAQLRV 108
 Db 209 RRSGCARPRAAGTQGRGLHAPRPRGRRALRL 248

RESULT 5
US-10-47-963-109275
*; Sequence 109275, Application US/10437963
 ; Publication No. US2004123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(5321)B
 ; CURRENT APPLICATION NUMBER: US/10/437, 963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 202661
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1) (311)
 ; OTHER INFORMATION: unsure at all xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_9791C.1.pep
 US-10-437-963-202661*

Query Match 13.7%; Score 108.5; DB 16; Length 311;
 Best Local Similarity 27.7%; Prod. No. 0.5;
 Matches 44; Conservative 13; Mismatches 67; Indels 35; Gaps 8;

Qy 20 PGSHRSRSLGGDPRPV-----KPRPDP--ARSPSSSLQPRHPA PR--PVVWKLR 64

SEQ ID NO: 109275
*i LENGTH: 413
 i TYPE: PRT
 i ORGANISM: Oryza sativa
 i FEATURE:
 i OTHER INFORMATION: Clone ID: PAT_MRT4530_13448C.1.pep*
 US-10-437-963-109275
 Query Match 13.2%; Score 105; DB 16; Length 413;
 Best Local Similarity 28.8%; Pred. No. 1.3; Mismatches 57; Indels 74; Gaps 12;
 Matches 57; Conservative 15; N mismatches 52; Delins 52; Length: 179
 SEQ ID NO: 3 RIPTAALGCSLICLQLPGLSLSRSL--GADPDPYKPREPPARSPSSSIQPRH-----
 Db 6 RLAGALGCSLFL----LSRALNFSQDPEPK---RPDEASSISUPDRIAIIAA 56
 Qy 53 PAPRPyVVKHERALQORGIGLAPYM----GOPLRDGGR-----
 Qy 57 PAPSP-----ATAAASDGSAPAQDEVRCDLFDSWYDPAQYPLVYAGECPFLSDQY 109
 Qy 88 --QHSGPPIRSQG-----BRRTQALQ-LRGCVLGTQVQ-----NISHREIWO-----
 Db 110 TCRRG-RPSGYEHTWRQPRCAALRGGEMLEQRDRDKRVVLTGDSLNRNWESLAC 168
 Qy 127 -LMGPAGRDQSPAPYDFSS 143
 Db 169 ILYAAPDPDRATVDAS 186
 RESULT 6
 US-10-425-114-64514
 ; Sequence 64514, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-18
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO: 64514
 ; LENGTH: 556
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3066-032-G9_FLI.pep
 US-10-425-114-64514
 Query Match 13.0%; Score 103; DB 15; Length 556;
 Best Local Similarity 28.0%; Pred. No. 2.5; Mismatches 44; Indels 50; Gaps 7;
 Matches 44; Conservative 18; N mismatches 45; Delins 50; Length: 242
 SEQ ID NO: 17 LQLPGSLSR--SLGGDPRTKPREPPARSPSSSIQPRHAPRPyVVKHLRHALQORG--
 Db 53 LRLPQAQRPQAVHGDGR--QRDAQRAAGAHLPL-PPR-----HRPLRRGDLR 102
 Qy 72 -----AGLAPTMQPLRDGGQHSGSPRHSPPRTQAOQLVGVLTGCOV 117
 Db 103 PAQHPGGPRLAHPAGRGGDGRLLRRGHRALRDRPAPRGRARLQLHALPFGAVAV 162
 Qy 118 QNLSHRLWQMGPAQDSSQPRDGGQHSGSPRHSPPRTQAOQLVGVLTGCOV 117
 Db 163 V-----QDADLPAPRGGRGQPHGIG 184
 RESULT 7
 US-10-767-701-35404

; Sequence 35404, Application US/10767701
 ; Publication No. US20040172684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5335)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO: 35404
 ; LENGTH: 179
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(179)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-066925_1.pep
 US-10-767-701-35404
 Query Match 12.8%; Score 101.5; DB 16; Length 179;
 Best Local Similarity 32.2%; Pred. No. 1.1; Mismatches 41; Indels 37; Gaps 6;
 Matches 39; Conservative 4; Software: FastSSQ for Windows Version 3.0
 Qy 31 PRPVKPREPPARSPSSSIQPRHAPRPyVVKHLRHALQORGAGLAPVMGQPLRDGGRQHS 90
 Db 80 PRPAPPERRPPXPXERA-PESPPAPPAPPA-----APRGEGPAP-----PRARCGARRH 126
 Qy 91 GPRHS-----SPRITAQLRQVGVLTGTCQVNLSHLWQLMQGAPRQDSAPVPDSS 143
 Db 127 VPRAAARAAPAPGQPRRPLPAQRCRRG-----RPRLGAAGGGCRGP-----PRS 169
 Qy 144 P 144
 Db 170 P 170
 RESULT 8
 US-10-450-436-28
 ; Sequence 64514, Application US/10450436
 ; Publication No. US20040077832A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Jian
 ; APPLICANT: Kinzler, Kenneth
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: JFY1 induces rapid apoptosis
 ; FILE REFERENCE: 01107.00062
 ; CURRENT APPLICATION NUMBER: US/10/450,436
 ; CURRENT FILING DATE: 2003-06-18
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSSQ for Windows Version 3.0
 ; SEQ ID NO: 28
 ; LENGTH: 242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: Clone ID: LIB3066-032-G9_FLI.pep
 US-10-450-436-28
 Query Match 12.7%; Score 101; DB 15; Length 242;
 Best Local Similarity 23.7%; Pred. No. 1.6; Mismatches 57; Indels 36; Gaps 7;
 Matches 43; Conservative 9; Software: FastSSQ for Windows Version 3.0
 Qy 18 QLPGSLSRSLGQPLRDGGQHSGSPRHSPPRTQAOQLVGVLTGCOV 117
 Db 24 QLPGARR-----GRCPRRPAPlPARPGALGVSILRPLARPGRPHPAARClPLRPH 78
 Qy 64 RALOQORGAGLAPNGQPLRDGGQHSGSPRHSPPRTQAOQLVGVLTGCOV 117
 Db 79 RPTRHRRPG-----GPFLAWGSPQ-----PAPRPAQRSSALAGGAAPGVARAPQPG-- 128

QY 124 LWQLMGPAGRQDSAPVDPSSSPHSYGV 148
 Db 129 ----GSGGR--SPPGGPESPRGEG 146

RESULT 9
 US-10-767-701-34727
 ; Sequence 3:727, Application US/10767701
 ; GENERAL INFORMATION:
 ; Publication No. US200400172684A1
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
 ; FILE REFERENCE: 38-21(53535)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO: 34727
 ; LENGTH: 203
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: SORBI-28WAY03-C53158_1.pep
 US-10-767-701-34727

Query Match 12.5%; Score 99.5; DB 16; Length 203;
 Best Local Similarity 30.4%; Pred. No. 1.8;
 Matches 41; Conservative 10; Mismatches 43; Indels 41; Gaps 8;

QY 17 LQL--PGSLRSLGDDP-RPUVDPREPAPARSPSSSLQPHPARPVVTKHLQA--Q 69
 Db 12 LQLSPPOCPQRSTAGAPRPARVHRPGG-----PPEPPPPAPPAHPDCHGCCID 64
 QY 70 RGAGIAPNGQP-----LIRDGRQHSGPRRHSGRR-----TQAQLRVG 109
 Db 65 GGAGAAPRPRPRAAPALPRLRDG----GFDRGGGPROPLKRTMTNTSQIARVG 119

QY 110 CVLGTCQYONLSHL 124
 Db 120 A--NVCPIDESDYEV 132

RESULT 10
 US-10-084-846A-6
 ; Sequence 6, Application US/10084846A
 ; Publication No. US20040000026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MOELLENWIG, AGNES
 ; APPLICANT: BECHTHOLD, AXEL
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO: 6
 ; LENGTH: 19662
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.
 ; OTHER INFORMATION: Start codon: 99a, Start position: nucleotide 1.
 US-10-084-846A-6

Query Match 12.5%; Score 99.5; DB 15; Length 19662;


```

Query Match      12.3%; Score 97.5; DB 14; Length 1003;
Best Local Similarity 23.3%; Pred. No. 13;
Matches 46; Conservative 17; Mismatches 67; Indels 27; Gaps 9;
Qy   6 TAALGCGISLICLQLPGSLRSLSLGADPR-PVTKPRAP-PAPS PSSSIQPRHHPA PPRPVWKLH 63
Db   791 SSPLACL-LOSLQIIPPEQPEAPCLPPEPSASALAPEAPPLSALAPPHGS PDPFPVPELL 849

Qy   64 RALQQR----GAGLAPMNGQPLRDGGGRHSGSPRRHSCEPRRTQAQLLRVGCVLGT----- 114
Db   850 TGRGGKGRGERGGGLRGINGEARDARGRK-PGSREPG-----RLALKNGTRGGF 899

Qy   115 -CQYONLSHRL-WQLMGPAGRQDSAPVD-PSSPHS 146
Db   900 NGQWERSPRTHHQHNGELAEGGAEPKDOPPPPCPHS 936

Search completed: October 22, 2004, 09:06:05
Job time : 130 secs

```

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	Pseudomon
protein - protein search, using sw model		
on:	October 22, 2004, 08:37:31 ; Search time 154 Seconds (without alignments) 344,753 Million cell updates/sec	
title:	US-10-723-368-2	
perfect score:	794	
Sequence:	1 MARIPTAAUGCISIUCILQLP.....GPAQRQDSAPVDPSSPHSYG 148	
Scoring table:	BLOSUM62	
Gapext:	0.5	
searched:	2002273 seqs, 35872999 residues	

ALIGNMENTS

```
st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARIES							Description
	%	Query No.	Score	Match Length	DB ID	ID	
1	794	100.0	148	8	AD061520	Human.int	Ado61520
2	254	32.0	47	8	AD061523	Human.int	Ado61523
3	110	13.9	379	7	Abo78178	Pseudomon	Abo78178
4	108	13.6	362	7	Abo82895	Pseudomon	Abo82895
5	107.5	13.5	514	7	ABO79462	Pseudomon	Abo79462
6	103.5	13.0	621	7	ABO81943	Pseudomon	Abo81943
7	103.5	13.0	1993	6	AB898398	StereoCony	Ab898398
8	103	13.0	142	7	ABO72835	Pseudomon	Abo72835
9	102.5	12.9	417	7	ABO75295	Pseudomon	Abo75295
10	101	12.7	242	3	AA9Y96318	Mammalian	Aay96318
11	101	12.7	242	5	ABG32397	Human.JFY	Abg32397
12	101	12.7	327	2	ABO82202	Pseudomon	Abo82202
13	100.5	12.7	528	7	ABO61540	Pseudomon	Ado61540
14	100	12.6	464	7	ABO7087	Pseudomon	Abo7087
15	100	12.6	555	4	ABG16571	Novel.hum	Abg16571
16	100	12.6	783	7	ABO69289	Pseudomon	Ado69289
17	99.5	12.5	763	7	ABO81400	Pseudomon	Abo81400
18	99	12.5	373	7	ABO76215	Pseudomon	Abo76215
19	99	12.5	588	7	ABO81944	Pseudomon	Ado81944
20	98.5	12.4	176	7	ABO81796	Pseudomon	Abo81796
21	98.5	12.4	275	7	ABO75230	Pseudomon	Abo75230
22	98.5	12.4	307	4	ABG04221	Novel.hum	Abg04221
23	98.5	12.4	362	7	ABO82270	Pseudomon	Abo82270
24	98.5	12.4	364	7	ABO71177	Pseudomon	Abo71177
25	98.5	12.4	160	7	ABO75220	Pseudomon	Abo75220

THE HISTORICAL JOURNAL OF THE AMERICAN REVOLUTION

pituitary, or for ovarian follicle survival and growth. They are also useful in the reduction of oedema. The present sequence represents the human intermedin protein of the invention.

ID	ABO72835 standard; protein; 142 AA.	XX	Pseudomonas aeruginosa polypeptide #7470.
AC	ABO72835;	XX	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
DT	29-JUL-2004 (first entry)	XX	
XX	Pseudomonas aeruginosa polypeptide #5010.	XX	
DE	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.	XX	
KW	Pseudomonas aeruginosa.	XX	
XX	Pseudomonas aeruginosa.	XX	
OS	Pseudomonas aeruginosa.	XX	
XX	Pseudomonas aeruginosa.	XX	
PN	US6551795-B1.	XX	
XX	US6551795-B1.	XX	
PD	22-APR-2003.	XX	
XX	22-APR-2003.	XX	
PP	18-FEB-1999; 99US-00252991.	XX	
XX	18-FEB-1999; 99US-00252991.	XX	
PR	18-FEB-1998; 98US-0074788P.	XX	
PR	27-JUL-1998; 98US-0094190P.	XX	
XX	98US-0094190P.	XX	
PA	(GENO-) GENOME THERAPEUTICS CORP.	XX	
XX	(GENO-) GENOME THERAPEUTICS CORP.	XX	
PI	Rubenfield MJ, Nolling J, Deloughery C, Bush D;	XX	
XX	Rubenfield MJ, Nolling J, Deloughery C, Bush D;	XX	
WPI	2003-615309/58.	XX	
DR	N-PSBB; ABD06406.	XX	
PT	Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.	XX	
PS	Disclosure: SEQ ID NO 24041; 455pp; English.	XX	
PT	The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for recombinant drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biotech technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html	CC	
XX	SEQ ID NO 21581; 455pp; English.	XX	
PT	Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.	XX	
PS	Disclosure: SEQ ID NO 21581; 455pp; English.	XX	
CC	The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for recombinant drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biotech technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patient did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html	CC	
XX	Sequence 142 AA;	XX	
SO	Query Match Score 102.5; DB 7; Length 417;	XX	
Best Local Similarity 27.9%; Pred. No. 0.32;	XX		
Matches 36; Conservative 8; Mismatches 58; Indels 27; Gaps 3;	XX		
QY	20 PGSLRSICGDPREPKPREPPARSPSSSTQPRHHPAPRPVWKLHRLAQORGAGLAPYM 78	Db	
Db	216 PGSGTHRALYGDHPHPAGSADAAPSQSRAPAAHPVPCARRRLUSTGGGKPGGRFRPGI 275	Db	
QY	79 -----GQPEDRGGRQHSGRQHSGRHSPRRTAQQLRVRGCTVQNLHRLWLMGPAG 132	Db	
Db	276 PRSAPPGHPPYSRGPPDPGDRRPLHRPRR-----	Db	
QY	133 RDSSAFAVDP 141	Db	
Db	316 PGRLILVVRP 324	Db	
RESULT 10			
RESLT 9			
ABO7295	AAV96318		
ID	AAV96318 standard; protein; 417 AA.		
XX	AAV96318;		
AC	AAV96318;		
XX	AAV96318;		
DT	17-AUG-2000 (first entry)		
XX			

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX

PS Disclosure: SEQ ID NO 30948; 455PP; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infections, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX

Sequence 327 AA;

Query	11	CISLICLQPGCSLSRLGDPVRK-----PREPPARSPSS-----	Score 101; DB 7; Length 327;
Best Local Similarity	30.2%	Pred. No. 0.34;	Indels 54; Gaps 11;
Matches	54	Conservative 15; Mismatches 58;	Gaps 11;
Db	55	CLPLLRRTTIAAGHQGGPKAVAAAGAGRPRVAVLRCRPLAAGAPGACDRRGR 114	
Qy	47	--SLOPRPA---PRPVWKLHRA-1QAQRGAGA- PVMGQLRDRGQRHSG- PR 93	
Db	115	GRALSRPRAAGCQEQP----FRAGURARRAAGLACPPATSRRLAAGRRGTVGLHPA 169	
Qy	94	RHSG----PRTOQOLLRGCVLGTICQYDNLSHRIWQINGPAGEQDSAVPD---PSSP 144	
Db	170	VEPGGLYQPRTRIDRALVQVLRPGRCAALRPRRTAAVAG-AGRA-ARPVDGQWPGP 226	

XX Query Match 12.7%; Score 101; DB 7; Length 528;
 XX Best Local Similarity 28.0%; Pred. No. 0.63;
 XX Matches 47; Conservative 9; Mismatches 43; Indels 69; Gaps 9;
 XX Qy 28 GGDPVRVPK-----REPPARSPSSLO---PRHPAPRPPVVKLHLR 66
 XX Db 52 GDDPYTADEPRRGANTPAIGHPAGGGADLROPAAAULPGALHLPVPRHPAVVLLHRL 111
 XX Qy 67 QAQ----RGAGLAPMNGQPIR--DGG----RQHSSEPRHISGPRRT 101
 XX Db 112 QPBCHTRPGLSQRVLPRLQHGLCLR----QHRLHDGTLRRDQEHAAPRSSGARLR 168
 XX Qy 102 QAQL---LRYGCVLTGICQVONIS-----HRLWQLMGP 131
 XX Db 169 HGRLLPILPAHRPALGAAPTAGVLOQRSDPDAFHIGGVHR--HSAGGA 214
 XX Sequence 528 AA;

RESULT 14
 ABO77087
 ID ABO77087 standard; protein; 464 AA.
 XX AC ABO77087;
 XX DT 29-JUL-2004 (first entry)
 XX DE Pseudomonas aeruginosa polypeptide #9262.
 XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX OS Pseudomonas aeruginosa.
 XX PN US6551795-B1.
 XX PD 22-APR-2003.
 XX PP 18-FEB-1999; 99US-00252991.
 XX PR 18-FEB-1998; 98US-0074788P.
 XX PR 27-JUL-1998; 98US-0094190P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX DR WPI; 2003-615309/58.
 XX DR N-PSDB; ABD03111.
 XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

Disclosure; SEQ ID NO 25833; 455pp; English.

The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant products of *P. aeruginosa*-derived peptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biotech technology. Sequences AB06/826-AB04396 represent *P. aeruginosa* polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqata.uspto.gov/sequence.html

XX Sequence 464 AA;

Query Match 12.6%; Score 100; DB 7; Length 464;
Best Local Similarity 28.4%; Pred. No. 0.61; Mismatches 13; Indels 46; Gaps 9;

Matches 42; Conservative 13; N mismatches 47; Indels 46; Gaps 9;

XX Sequence 555 AA;

QY 29 GDP-RPVK---PREPPARSPSSSLQPRHFA----PRPVWKLHRLAQARQA 72

Db 185 GDPHRPGRRVPGPADAAPAARGRNQPROFGDRHCAAAYAGHPAPAVLRLHSQRHRSR 244

QY 73 GLAPVNGQPLR-----DGGRQHSPPRHSGPRITQAQLLRVGCVLGLTCQVNQLS 121

Db 245 ARGP---RPRVQRAGDADAPADPQRH---RRNGLRR-RRQLPR-----PVEGTD 290

QY 122 HRLW---QLMGPAGRQDSAPVDPSSP 144

Db 291 RRAWPGRHRLEPEPQRGPAYHGP 318

RESULT 15
ID ABG16571 standard; protein; 555 AA.
XX ABG16571;
AC XX
DT 18-FEB-2002 (first entry)
DE Novel human diagnostic protein #16562.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
PN XX
PD XX
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX (HYSEQ) HYSEQ INC.
PA XX
PT Drmanac RT, Liu C, Tang YT;
XX DR; 2001-639362/73.
DR N-PDB; AAS80758.
PT New isolated polynucleotide and encoded polypeptides, useful in

diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

XX

PS

XX

Claim 20; SEQ ID NO 46930; 103pp; English.

XX

PS

XX

The invention relates to isolated polynucleotide (I) and polypeptide (II).

CC

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 08:46:06 ; Search time 37 Seconds

(without alignments)
 384.867 Million cell updates/sec

Title: US-10-723-368-2
 Perfect score: 794
 Sequence: 1 MARIPPAALGCTISLLCQLQP.....GPAGRQDSAPVDPSSPHSYG 148

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79;*

1: Pir1;*
 2: Pir2;*
 3: Pir3;*
 4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93.5	11.8	220	2 T50624	hypothetical prote
2	93.5	11.8	414	2 C6301	arginine/serine-ri
3	91.5	11.5	309	2 S10889	proline-rich prote
4	91	11.5	220	2 A36298	proline-rich prote
5	90	11.3	170	2 B57663	oligodendrocyte-sp
6	89.5	11.3	706	2 B30411	synapsin Ia - bovi
7	88.5	11.1	221	2 B48266	protein-tyrosine k
8	88	11	304	2 T29421	hypothetical prote
9	87.5	11.0	308	2 E70885	lysostaphin - Syne
10	87.5	11.0	411	2 S75327	immediate-early pr
11	87	11.0	676	1 EDBE23	hypothetical prote
12	86.5	10.9	226	2 S33024	immediate-early pr
13	86.5	10.9	1460	1 EDBE1F	proline-rich prote
14	86	10.8	212	2 C86301	gene BCREF2 protein
15	86	10.8	383	2 S23298	arginine/serine-rich protein [imported] - Arabidopsis thaliana
16	86	10.8	676	1 EDBE22	C;Species: Arabidopsis thaliana 'mouse ear cress'
17	85.5	10.8	322	2 T22403	C;Accession: 02-Mar-2001 #sequence_revision 02-Mar-2001
18	85.5	10.8	381	2 S216506	C;Change: 09-Jul-2004
19	85.5	10.8	847	1 A53800	R;InSeqlis, A.; Ecker, J.R.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, R;Authors: Hunter, J.L.; Jenkins, C.J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
20	85.5	10.8	1734	2 A54602	A;Authors: Salzberg, S.L.; Schwarz, P.; Shinn, P.; Southwick, A.M.; Sun, H.; Talton, J.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
21	85.5	10.8	1870	2 S31671	A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
22	85.5	10.8	236152	2 S31653	A;Reference number: A86141; PMID:1130712
23	84.5	10.6	705	2 A53363	
24	84.5	10.6	864	2 A88266	
25	84.5	10.6	975	2 S3121	
26	84.5	10.6	1217	2 T22625	
27	84	10.6	2142	2 B35098	
28	84	10.6	640	2 T08179	
29	84	10.6	825	2 JC4163	

RESULT 1

T50624

hypothetical protein DKFP762N1313.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000

C;Accession: T50624

R;Ansorge, W.; Wirkner, U.; Newes, H.W.; Weil, B.; Wiemann, S.

Submitted to the Protein Sequence Database, June 2000

A;Reference number: 225142

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-220 <AAs>

A;Cross-references: EMBL:AL359594

A;Experimental source: adult melanoma (MeWo cell line); clone DKFP762N1313.1

C;Genetics:

A;Note: DKFP762N1313.1

Query Match 11.8%; Score 93.5; DB 2; Length: 220;

Best Local Similarity 28.4%; Pred. No. 0.88;

Matches 44; Conservative 20; Mismatches 66; Indels 25; Gaps 7;

Query 6 TAALGGSISLCLQLGQSLSRLGGDPR-PARSPPSSSLQPRHPPAPRPPVWKLUH 63

Db 59 SSPLAIC-LQSLQIPEQOPAPCILPESPALEPPARPPSALSALAPHGSPDPVPPPELL 117

Qy 64 RALQACR----GAGIAAPNGQPLDGRGQHESGPGRHSG-----PRTOQA 103

Db 118 TGRGSCKRGRGGGGGRRGNGEARPARGRK-PGSRREPGRLALKWTRGGFNGOMERSQEE 176

Qy 104 QLLRVCVLNCQYONLSHIWQMGPAHQDSAP 13B

Db 177 E-PTGSISSWIKGVTSPIHPLFQPIRLTRLCP 210

RESULT 2

C86301

arginine/serine-rich protein [imported]

C;Species: Arabidopsis thaliana (mouse ear cress)

C;Accession: 02-Mar-2001 #sequence_revision 02-Mar-2001

C;Change: 09-Jul-2004

R;InSeqlis, A.; Ecker, J.R.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, R;Authors: Hunter, J.L.; Jenkins, C.J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Nature 406, 816-820, 2000

A;Authors: Ansorge, W.; Wirkner, U.; Newes, H.W.; Weil, B.; Wiemann, S.; Huizar, L.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana (mouse ear cress)

A;Reference number: A86141; PMID:1130712

A;Residues: 1-706 <SUE>
A;Accession: F30411
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-661 ;KA-, 661 , 'PAQAP', <SU2>
R;Hall, F.L.; Mitchell, J.P.; Vuilliet, P.R.
J. Biol. Chem. 265, 6944-6948, 1990
A;Title: Phosphorylation of synapsin I at a novel site by proline-directed protein kinase
A;Reference number: A35758 ; MUID:90216728 ; PMID:2108963
A;Accession: A35758
A;Molecule type: protein
A;Residues: 532-556 <HAL>
C;Keywords: actin binding; alternative splicing; phosphoprotein
F;551/Binding site: phosphate (Ser) (covalent) (by proline-directed kinase) #status exper

Query Match 11.3%; Score 89.5; DB 2; Length 706;
Best Local Similarity 29.3%; Pred. No. 5.5; Gaps 8;
Matches 41; Conservative 15; Mismatches 51; Indels 33; Gaps 8;

Qy 18 QLPGS---LRSLSLGDPVK--PREPAPRSPSSSLQPPHPAPPVWKLHRAHQAG 71
Db 516 QQPASQATPMTQGQGRQSRVYAGGFPAAPPTRPASPSPQRQAFPP----QATROTSEV 569
Qy 72 AGLAPVMGQPLRDGGRRH---SGPRRTAQ---LLRVCVILNCVQVNLSHL 124
Db 570 SGQADPKASVPPGGQQRPQPPQRQPGPAGQPTQASQAGMPRTG--PPTTQQRPSG-- 625
Qy 125 WQLMGPAQRDSDASAPVDPSSP 144
Db 626 ---PSPAGR-----PTXP 635

RESULT 7

B48266
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 29-Aug-1997
C;Accession: B48266
R;Toyoshima, H.; Kozutsumi, H.; Maru, Y.; Hagiwara, K.; Furuya, A.; Mioh, H.; Hanai, N./
Proc. Natl. Acad. Sci. U.S.A. 90, 5404-5408, 1993
A;Title: Differently spliced cDNAs of human leukocyte tyrosine kinase receptor tyrosine
A;Reference number: A48266 ; MUID:93296146 ; PMID:7685902
A;Accession: B48266
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-221 <TOY>
A;Experimental source: placenta
A;Note: sequence inconsistent with nucleotide translation
C;Genetics:
A;Gene: GDB:1277668 ; OMIM:151520
A;Map position: 15q15.1-15q15.2

Query Match 11.1%; Score 88.5; DB 2; Length 221;
Best Local Similarity 28.9%; Pred. No. 2.3; Gaps 8;
Matches 37; Conservative 11; Mismatches 43; Indels 37; Gaps 8;

Qy 13 SLLCQLPGSLSRLGGDPVK--KPREPPARSPPSSSIQPRHHPAPPVWKLHRAHQAG 69
Db 16 AILC-SSPGQBTELRSSPLASPRDKVSAQSPSILEPASLNSP-----GT 64

Qy 70 RGAGLAPVMGQPLRDGGRRHQSGRHSGPRRTAQQLRVGCVLGTQV----QNLSH 122
Db 65 EGSQLWLFSTCGA-----SG-RH-GPTQTQCD---GAYAGTSVVVTGAAQOLRGV 108
Qy 123 RLWQLMGP 130
Db 109 QLWRVPEP 116

RESULT 9

E70885
hypothetical protein Rv2859c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E70885
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feilwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 399, 537-544, 1998
A;Author: Spokes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome : A;Reference number: A70800 ; MUID:98295587 ; PMID:9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-308 <COL>
A;Cross-references: UNIPROT:033341 ; GB:AL008883 ; GB:AL123456 ; NID:g3261490 ; PIDN:CAA1552;
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv2859c

Query Match 11.0%; Score 87.5; DB 2; Length 308;
Best Local Similarity 27.5%; Pred. No. 3.7;
Matches 39; Conservative 15; Mismatches 39; Indels 49; Gaps 8;

Qy 22 SLSRSITGGDPVKPRPPARSP-SSSLQPRHHPAPPVWKLHRAHQAGLAQFMGQ 80
Db 4 SASRSPGGD-PLRASPSPRSPVDDGGDPLRPA-----SPRLRS 41

Qy 81 PLRDGGRRHQSGRHSGPRRTAQQLRVGCVLGTQV-TQVQNLSHRLWQLMGPAGQDS--- 136
Db 42 PVSDGG---DPLRASP-KLRSPLAGASREVGLTAYLEQVRTGTVWDI-PAGYLPAFY 94

RESULT 10

T29421

EGITMAGGVAVLPPQPVDPES 11.6

lysostaphin - Synechocystis sp. (strain PCC 6803)
 N;Alternate names: Proton SLR1708
 C;Species: Synechocystis sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S75327
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O.; Kurokawa, K.; Shimizu, S.; Takeuchi, C.; Wada, T.; Watanaabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
 A;Reference number: S74322; MUID:97061201; PMID:1905331
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-411 <KAN>
 A;Cross-references: UNIPROT:P73214; EMBL:D90904; GB:AB001339; NID:91652225; PIDN:BAA1724
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match	11.0%	Score 87.5;	DB 2;	Length 411;
Best Local Similarity	27.0%	Pred. No. 4.9;	Mismatches 19;	Indels 57; Gaps 11;
Matches	47;	Conservative	19;	

QY 2 ARIPTAAG--CISLCLQIQLPGLSRL--GGDPPIPKPREPPA-----RSP 44
 Db 18 ANLYNLISGLIIGLGVNSLPGTTGNLEIEQSAPAPTPAAPVKAQPVQSVIP 77

QY 45 SSS-LQPRHAPRPVWKLHLRQLQQRGAGLAPNGQP--LRDGROHS---GPRRSY 97
 Db 78 DSKPDAPIRPAAPT-----IAPISSQAOIQRLQGKNTYDAAQPGTAA 120

QY 98 ---PRRTQAOQLL-RVGCVLGTGTCQVQNLSHRLWQL---MGPAQRODASAPVDP 141
 Db 121 APNLSTRTEVEFVPRSG----QQAPINTRYPAANRASPQAROQSSPVNP 168

RESULT 11
 EDDB23 immediate-early protein IER2.9 - bovine herpesvirus 1 (strain Jura)
 N;Alternate names: early protein ER2.6; p135 protein
 C;Species: bovine herpesvirus 1
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C;Accession: B38209
 R;Wirth, U.V.; Freefel, C.; Vogt, B.; Vlcek, C.; Paces, V.; Schwyzter, M.
 J.Virol. 66, 2763-2772, 1992
 A;Title: Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 are 3' coterminal
 A;Reference number: B38209; MUID:92219360; PMID:1313901
 A;Accession: B38209
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:P29128; GB:M84465; NID:9330769; PIDN:AAA46062.1; PID:9330770
 C;Supplementary information: herpesvirus immediate-early protein IE110; RING finger homology
 F;9-57/Domain: RING finger homology <RNG>
 F;13-51/Region: zinc finger C3HC4 motif
 F;284-311/Region: acidic

Query Match	11.0%	Score 87;	DB 1;	Length 676;
Best Local Similarity	33.3%	Pred. No. 8.4;	Mismatches 8;	Indels 30; Gaps 8;
Matches	39;	Conservative	8;	

QY 1 MARIPTAAGCISLCLQIQLPGLSRLSLOGG--DPR-PVKPREPPARSPSSSLQPRHPAPR 57
 Db 369 LAKRPCCGRARVS----APPS-SRSRGGRDPLPAAPRAATA----AQARACSEPEP 416

QY 58 VVVKHLRQLAOQAGAIAQPMGQPL--RDGGRQHSQGPRR----HSGPERTQOQLR 107
 Db 417 -----REBEGRAGLGVAAGETAGWAGAGSEEGERRARRLGEAAGRPRVQARR 465

RESULT 12
 S33024 hypothetical protein - human herpesvirus 4

C;Species: human herpesvirus 4, Epstein-Barr virus
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C;Accession: S33024
 R;Farrell, P.J.
 submitted to the EMBL Data Library, March 1988
 A;Reference number: S32973
 A;Accession: S33024
 A;Molecule type: DNA
 A;Residues: 1-226 <FAR>
 A;Cross-references: EMBL:V01555

Query Match	10.9%	Score 86.5;	DB 2;	Length 226;
Best Local Similarity	30.2%	Pred. No. 3.4;	Mismatches 7;	Indels 47; Gaps 7;
Matches	38;	Conservative	7;	

QY 22 SLSRSLLGDDBRPVKPREPPARSPSSSLQPRHPAPRPPVWKLHLRQLAOQAGAIAQPMGQPL 81
 Db 126 STQOSSGLTPTPSR-PRTRAP-----PRPPAPAV-----RGRASAP-----P 164

QY 82 LRDGQRQHSPCPRSSGPRRTQAQQLRVCGLTGQVQNLSHRLWQLMGPAQROSAPVDP 141
 Db 165 RPPAPVQQS-TKDGPHRPTPRVPLR-----GPAPRR---PPPP 198

RESULT 13
 EDDB1F immediate-early protein IE160 - suis herpesvirus 1 (strain Indiana-Funkhauser)
 C;Species: suis herpesvirus 1
 C;Accession: S04713
 C;Sequence revision 30-Jun-1990 #text_change 09-Jul-2004

R;Cheung, A.K.
 Nucleic Acids Res. 17, 4637-4646, 1989
 A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies virus
 A;Reference number: S04713; PMID:8931207; PMID:2546124

QY 18 QLPSSLSRLSLLGDDBRPVKPREPPARSPSSSLQPRHPAPRPPVWKLHLRQLAOQAGAIAF 77
 Db 157 QRPEHP-PAAPGARDPQOPERPQPPAPP-----RPPAPP-----RPPRDG-----RPPRDG 198

QY 78 MGQLJRDGERQHS-GPRRHSGPRTQAOQLRVGGVILGTCQVNQNLSHRLWQLMGPAQRODS 136
 Db 199 ---PPRGTRTSVSGRRGCLGPQRHQH-----SQQRW-----PQRHIGG 234

RESULT 14
 B32298 proline-rich protein PRB3S (cys) - human (fragment)
 C;Species: Homo sapiens (mbo)
 C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
 C;Accession: B36298
 R;Azen, B.A.; Minaguchi, K.; Latreille, P.; Kim, H.S.
 Am. J. Hum. Genet. 47, 686-697, 1990
 A;Title: Alleles at the PRB3 locus coding for a disulfide-bonded human salivary proline
 A;Reference number: A36298; MUID:91022705; PMID:2171329

Search completed: October 22, 2004, 08:55:12
Job time : 40 secs

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A;Accession: S02383
 A;Molecule type: DNA
 A;Residues: 88-144 <WAL>
 A;Cross-references: EMBL:X07816
 C;Genetics:
 A;Name: BMRP1_2; BMRP1_3; BMRP1_4; BMRP1_5; BMRP1_6; BMRP1_7; BMRP1_8; BMRP1_9;
 A;Note: twelve consecutive ORFs apparently encode the identical polypeptide
 C;Superfamily: proline-rich protein
 A;

Query	Match	Score	DB	Length
Qy	CISHCQLPGSSLRSLSGDPRKWP--REPPA-RSPSSSLOPRHPAPRPVTKLHRALQ	67		383
Ddb	CPSLCPSSEPGT-----SGTPEPIGLPARRRPGIERSPSVPEK-----	92		131
Qy	AQRAGL--AP-----VNGQPLRGGHQSQGPRR-	68		94
Ddb	CLRAATLGAAQAPERSRGQGHLLRVPRVPEQGP--EGPRQGRPVRPVRPFQGIQSPGCPPE	132		189
Qy	-----HSGPRTTQJQLLRGGVLTGTCQVNLISRLWQMGPAQRQDASAPVDPSSP	95		144
Ddb	GMIACVPSPPDQCARSPSPRGASQGP-OVO-PEP-----	190		225

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